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Wed Aug 22 08:39:01 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
Repeats masked (summary below)
/home/ruby/va/Molbio/carpenda/tempids/ss.DNA44804 (2555 bp)

MAY 29 2002

TECH CENTER 1600/2900

BLAST RESULTS AT

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-val
1	P_AAA49564 Human PRO357 cDNA.	+	2555	2555	100	0.0
2	P_AAA46922 cDNA encoding novel polypeptide PRO357.	+	2555	2555	100	0.0
3	P_AAX80056 Human PRO357 nucleotide sequence.	+	2555	2555	100	0.0
4	P_AAX87261 cDNA clone encoding human PRO357, amplif	+	2555	2555	100	0.0
5	P_AAA58765 cDNA encoding a leucine-rich surface gly	+	2142	2142	100	0.0
6	AC012676 Homo sapiens chromosome 16 clone RP11-29	+	2138	2141	100	0.0
7	AC005222 Homo sapiens chromosome 16, cosmid clone	+	2138	2141	100	0.0
8	P_AAF44105 Human PRO1282 (UNQ652) nucleotide sequen	+	2127	2139	100	0.0
9	P_AAF92065 Human PRO1282 cDNA.	+	2127	2139	100	0.0
10	P_AAZ64959 Membrane-bound protein PRO1282 encoding	+	2127	2139	100	0.0
11	AX092284 Sequence 15 from Patent WO0116318.	+	2127	2139	100	0.0
12	P_AAC69514 Human secreted protein gene 3 clone HSYA	+	2065	2135	99	0.0

>1 P_AAA49564 Human PRO357 cDNA. (2555 bp) [1 seg]

Score = 2555 (5065 bits), Expect = 0.0

Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

DNA44804	1	GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCC *****
P_AAA49564	1	GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCC
DNA44804	61	GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCCGCG *****
P_AAA49564	61	GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCCGCG
DNA44804	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTGCTGCTGCCGCTGCTCCTGCTACT *****
P_AAA49564	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTGCTGCTGCCGCTGCTCCTGCTACT
DNA44804	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGTGCAGCCAGCACAGAC *****
P_AAA49564	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGTGCAGCCAGCACAGAC
DNA44804	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT *****
P_AAA49564	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCT *****
P_AAA49564	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCT
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCCAGATCGCCAGCCTGCGCCTGCCCG *****
P_AAA49564	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCCAGATCGCCAGCCTGCGCCTGCCCG
DNA44804	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGA *****
P_AAA49564	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGA
DNA44804	481	CACTGCCAACGTGGAGGCCTGCGGCTGGCTGGCTGGGCTGCAGCAGCTGGACGAGGG

BLAST RESULTS A-2

P_AAA49564 481 CACTGCCAACGTGGAGGCCTGCGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGG
DNA44804 541 GCTCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCG

P_AAA49564 541 GCTCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCG
DNA44804 601 AGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCGCTGGCCGGCAACAC

P_AAA49564 601 AGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCGCTGGCCGGCAACAC
DNA44804 661 CGCGATTGCCAGCTGCGGCCAGGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA

P_AAA49564 661 CGCGATTGCCAGCTGCGGCCAGGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA
DNA44804 721 TGTGAGCAACCTAAGCCTGAGGCCCTGCCTGGCGACCTCTGGGCTCTTCCCCCGCCT

P_AAA49564 721 TGTGAGCAACCTAAGCCTGAGGCCCTGCCTGGCGACCTCTGGGCTCTTCCCCCGCCT
DNA44804 781 GCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGG

P_AAA49564 781 GCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGG
DNA44804 841 CCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT

P_AAA49564 841 CCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804 901 CCCGCCAAGAACGCTGGCGGCTGCTCCCTGGAGCTTGACTACGCCACTTGGCTGCC

P_AAA49564 901 CCCGCCAAGAACGCTGGCGGCTGCTCCCTGGAGCTTGACTACGCCACTTGGCTGCC
DNA44804 961 AGCCACCAACCACACAGCCACAGTGCCACCACGAGGCCGTGGTGCAGGGAGCCCACAGC

P_AAA49564 961 AGCCACCAACCACACAGCCACAGTGCCACCACGAGGCCGTGGTGCAGGGAGCCCACAGC
DNA44804 1021 CTTGTCTCTAGCTTGGCTCCTACCTGGTAGGCTAGCCCCACAGCGCCGGCACTGAGGCC

P_AAA49564 1021 CTTGTCTCTAGCTTGGCTCCTACCTGGTAGGCTAGCCCCACAGCGCCGGCACTGAGGCC
DNA44804 1081 CAGCCCGCCCTCACTGCCACCGACTGTAGGCCCTGTCCCCCAGCCCCAGGACTGCC

P_AAA49564 1081 CAGCCCGCCCTCACTGCCACCGACTGTAGGCCCTGTCCCCCAGCCCCAGGACTGCC
DNA44804 1141 ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG

P_AAA49564 1141 ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG
DNA44804 1201 CTTGTGCCCGAAGGCTCACGGCCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG

P_AAA49564 1201 CTTGTGCCCGAAGGCTCACGGCCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG
DNA44804 1261 GCCCAGCCCTACACCAAGTCACGCCAGGCCACCGTCCCTGACCCCTGGCATCGAGCC

P_AAA49564 1261 GCCCAGCCCTACACCAAGTCACGCCAGGCCACCGTCCCTGACCCCTGGCATCGAGCC
DNA44804 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCCAGGGAGCTCCGTGCA

BLAST RESULTS A3

P_AAA49564 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCCAGGGAGCTCCGTGCA
DNA44804 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGCCCTGATAAGCGGCTGGTGAC

P_AAA49564 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGCCCTGATAAGCGGCTGGTGAC
DNA44804 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGTCGGGCCAACGCCAC

P_AAA49564 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGTCGGGCCAACGCCAC
DNA44804 1501 TTACTCCGTCTGTGTCATGCCTTGGGCCGGCGGGTGCAGGAGGGCGAGGAGGCCTG

P_AAA49564 1501 TTACTCCGTCTGTGTCATGCCTTGGGCCGGCGGGTGCAGGAGGGCGAGGAGGCCTG
DNA44804 1561 CGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACCCAGGCCCG

P_AAA49564 1561 CGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACCCAGGCCCG
DNA44804 1621 CGAGGGCAACCTGCCGCTCCTCATTCGCCCCCTGGCGCGGTGCTCCTGGCGCGCT

P_AAA49564 1621 CGAGGGCAACCTGCCGCTCCTCATTCGCCCCCTGGCGCGGTGCTCCTGGCGCGCT
DNA44804 1681 GGCTGCGGTGGGGCAGCCTACTGTGTCGGCGGGGGCGGGCATGGCAGCAGCGGCTCA

P_AAA49564 1681 GGCTGCGGTGGGGCAGCCTACTGTGTCGGCGGGGGCGGGCATGGCAGCAGCGGCTCA
DNA44804 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAGGGAGTGAAGGTCCC

P_AAA49564 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAGGGAGTGAAGGTCCC
DNA44804 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA

P_AAA49564 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
DNA44804 1861 GTGTGAGGTGCCACTCATGGCCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA

P_AAA49564 1861 GTGTGAGGTGCCACTCATGGCCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA
DNA44804 1921 GCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA

P_AAA49564 1921 GCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA
DNA44804 1981 TGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCAACCTCGGGATGTG

P_AAA49564 1981 TGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCAACCTCGGGATGTG
DNA44804 2041 TGCAGACAGGGCTGTGACCAAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

P_AAA49564 2041 TGCAGACAGGGCTGTGACCAAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
DNA44804 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG

P_AAA49564 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCA

P_AAA49564 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCA

BLAST RESULTS A-4

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DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG
*****
P_AAA49564 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG

DNA44804 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
*****
P_AAA49564 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC

DNA44804 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAAAGAAACTGGAAAGGAAGATGCTTAGGAA
*****
P_AAA49564 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAAAGAAACTGGAAAGGAAGATGCTTAGGAA

DNA44804 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG
*****
P_AAA49564 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG

DNA44804 2461 GGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATA
*****
P_AAA49564 2461 GGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATA

DNA44804 2521 TGAAGGCCTTGTAAAGAAAAATAAAAAAAAAAAA
*****
P_AAA49564 2521 TGAAGGCCTTGTAAAGAAAAATAAAAAAAAAAAA

>2 P_AAA46922 cDNA encoding novel polypeptide PRO357. DNA, PAT 03-OCT-2000
(2555 bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

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DNA44804	1	GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
P_AAA46922	1	GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
DNA44804	61	GACCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGCTCCCTGCGCCGCCGCG
P_AAA46922	61	GACCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGCTCCCTGCGCCGCCGCG
DNA44804	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
P_AAA46922	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
DNA44804	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGAC
P_AAA46922	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGAC
DNA44804	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
P_AAA46922	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCCT
P_AAA46922	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCCT
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAAGATGCCAGCCTGCGCCTGCCCG
P_AAA46922	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAAGATGCCAGCCTGCGCCTGCCCG

BUAST RESULTS 4/5

DNA44804	421	CCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGA *****
P_AAA46922	421	CCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGA
DNA44804	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGG *****
P_AAA46922	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGG
DNA44804	541	GCTCTCAGCCGTTGCGAACCTCACGACCTGGATGTGTCGACAACCAGCTGGAGCG *****
P_AAA46922	541	GCTCTCAGCCGTTGCGAACCTCACGACCTGGATGTGTCGACAACCAGCTGGAGCG
DNA44804	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCTGCGCTGGCCGGCAACAC *****
P_AAA46922	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCTGCGCTGGCCGGCAACAC
DNA44804	661	CCGCATTGCCAGCTGCGCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA *****
P_AAA46922	661	CCGCATTGCCAGCTGCGCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA
DNA44804	721	TGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCCT *****
P_AAA46922	721	TGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCCT
DNA44804	781	GCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGG *****
P_AAA46922	781	GCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGG
DNA44804	841	CCCCTGGTGCAGAGGCCACGTACACTGGCAGCCCTGAGGAGACGCGCTGCCACTT *****
P_AAA46922	841	CCCCTGGTGCAGAGGCCACGTACACTGGCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804	901	CCCGCCAAGAACGCTGGCGGTGCTCTGGAGCTTGACTACGCCACTTGGCTGCC *****
P_AAA46922	901	CCCGCCAAGAACGCTGGCGGTGCTCTGGAGCTTGACTACGCCACTTGGCTGCC
DNA44804	961	AGCCACCACCAACCACAGCCACAGTGCCACACGAGGCCGTGGTGGAGCCACAGC *****
P_AAA46922	961	AGCCACCACCAACCACAGCCACAGTGCCACACGAGGCCGTGGTGGAGCCACAGC
DNA44804	1021	CTTGTCTCTAGCTTGGCTCTACCTGGCTAGCCCCACAGCGCCGGCCACTGAGGCC *****
P_AAA46922	1021	CTTGTCTCTAGCTTGGCTCTACCTGGCTAGCCCCACAGCGCCGGCCACTGAGGCC
DNA44804	1081	CAGCCGCCCTCCACTGCCACCGACTGTAGGGCTGTCCCCCAGCCCCAGGACTGCC *****
P_AAA46922	1081	CAGCCGCCCTCCACTGCCACCGACTGTAGGGCTGTCCCCCAGCCCCAGGACTGCC
DNA44804	1141	ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG *****
P_AAA46922	1141	ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG
DNA44804	1201	CTTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG *****
P_AAA46922	1201	CTTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG

BUST RESULTS A-1

DNA44804 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCTGGGCATCGAGCC

P AAA46922 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCTGGGCATCGAGCC

DNA44804 1321 GGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCACGCCAGGGAGCTCCGTGCA

P AAA46922 1321 GGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCACGCCAGGGAGCTCCGTGCA

DNA44804 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGCCCTGATAAGCGCTGGTGAC

P AAA46922 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGCCCTGATAAGCGCTGGTGAC

DNA44804 1441 GCTGCGACTGCCTGCCCTCGCTGAGTACACGGTCACCCAGCTGCCCAACGCCAC

P AAA46922 1441 GCTGCGACTGCCTGCCCTCGCTGAGTACACGGTCACCCAGCTGCCCAACGCCAC

DNA44804 1501 TTACTCCGTCTGTGTCATGCCATTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGGAGGCCTG

P AAA46922 1501 TTACTCCGTCTGTGTCATGCCATTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGGAGGCCTG

DNA44804 1561 CGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACCCAGGCCCG

P AAA46922 1561 CGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCAGTCACCCAGGCCCG

DNA44804 1621 CGAGGGCAACCTGCCGCTCCTCATTGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT

P AAA46922 1621 CGAGGGCAACCTGCCGCTCCTCATTGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT

DNA44804 1681 GGCTGCGGTGGGGCAGCCTACTGTGTGCCGGGGCGGGCATGGCAGCAGCGGCTCA

P AAA46922 1681 GGCTGCGGTGGGGCAGCCTACTGTGTGCCGGGGCGGGCATGGCAGCAGCGGCTCA

DNA44804 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTCCC

P AAA46922 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTCCC

DNA44804 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA

P AAA46922 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA

DNA44804 1861 GTGTGAGGTGCCACTCATGGCCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA

P AAA46922 1861 GTGTGAGGTGCCACTCATGGCCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA

DNA44804 1921 GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA

P AAA46922 1921 GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA

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DNA44804 2041 TGCAGACAGGGCTGTGACCAACAGCTGGGCCCTGTCCCTCTGGACCTCGGTCTCCTCA

P AAA46922 2041 TGCAGACAGGGCTGTGACCAACAGCTGGGCCCTGTCCCTCTGGACCTCGGTCTCCTCA

DNA44804 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCACCGAGGTGCCTATG

BLAST RESULTS A-7

P_AAA46922 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA
P_AAA46922 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA
DNA44804 2221 TGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG
P_AAA46922 2221 TGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG
DNA44804 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTC
P_AAA46922 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTC
DNA44804 2341 TAGTCTTGGCCCAGGAAGCGAAGGAACAAAGAAACTGGAAAGGAAGATGCTTAGGAA
P_AAA46922 2341 TAGTCTTGGCCCAGGAAGCGAAGGAACAAAGAAACTGGAAAGGAAGATGCTTAGGAA
DNA44804 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG
P_AAA46922 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG
DNA44804 2461 GGAAGATTTTCAAACACTCAGAGACAAGGACTTGGTTTTGTAAGACAAACGATGATA
P_AAA46922 2461 GGAAGATTTTCAAACACTCAGAGACAAGGACTTGGTTTTGTAAGACAAACGATGATA
DNA44804 2521 TGAAGGCCTTTGTAAGAAAAATAAAAAAAAAAAA
P_AAA46922 2521 TGAAGGCCTTTGTAAGAAAAATAAAAAAAAAAAA

>3 P_AAX80056 Human PRO357 nucleotide sequence. (2555 bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/-

DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTGCTTCGGGACCCAGGACCCCTCGGGCCC
P_AAX80056 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTGCTTCGGGACCCAGGACCCCTCGGGCCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCCGCG
P_AAX80056 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCCGCG
DNA44804 121 CCTCCCGGGACAGAAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
P_AAX80056 121 CCTCCCGGGACAGAAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
DNA44804 181 GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGAC
P_AAX80056 181 GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGAC
DNA44804 241 AGTCTTCTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
P_AAX80056 241 AGTCTTCTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804 301 GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCTGC

BLAST RESULTS A-B

P_AAX80056	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCTGGCCT
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGCGCCTGCCCG *****
P_AAX80056	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGCGCCTGCCCG
DNA44804	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGCCCTGGAGGCCGGCATCCTGGA *****
P_AAX80056	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGCCCTGGAGGCCGGCATCCTGGA
DNA44804	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGG *****
P_AAX80056	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGG
DNA44804	541	GCTCTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCG *****
P_AAX80056	541	GCTCTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCG
DNA44804	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCGGCTGGCCGGAACAC *****
P_AAX80056	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCGGCTGGCCGGAACAC
DNA44804	661	CCGCATTGCCAGCTGCGGCCAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA *****
P_AAX80056	661	CCGCATTGCCAGCTGCGGCCAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA
DNA44804	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCCT *****
P_AAX80056	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCCT
DNA44804	781	GCGGCTGCTGGCAGCTGCCGCAACCCCTTAAC TGCGTGTGCCCTGAGCTGGTTGG *****
P_AAX80056	781	GCGGCTGCTGGCAGCTGCCGCAACCCCTTAAC TGCGTGTGCCCTGAGCTGGTTGG
DNA44804	841	CCCCTGGTGCAGAGAGCCACGTACACTGCCAGCCCTGAGGAGACGCGCTGCCACTT *****
P_AAX80056	841	CCCCTGGTGCAGAGAGCCACGTACACTGCCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804	901	CCCGCCAAGAACGCTGGCCGGCTGCTCTGGAGCTTGACTACGCCACTTGGCTGCC *****
P_AAX80056	901	CCCGCCAAGAACGCTGGCCGGCTGCTCTGGAGCTTGACTACGCCACTTGGCTGCC
DNA44804	961	AGCCACCAACCACAGCCACAGTGCCACACGAGGCCGTGGTGGGGAGCCCACAGC *****
P_AAX80056	961	AGCCACCAACCACAGCCACAGTGCCACACGAGGCCGTGGTGGGGAGCCCACAGC
DNA44804	1021	CTTGTCTCTAGCTTGGCTCTACCTGGCTAGCCCCACAGCGCCGGCCACTGAGGCC *****
P_AAX80056	1021	CTTGTCTCTAGCTTGGCTCTACCTGGCTAGCCCCACAGCGCCGGCCACTGAGGCC
DNA44804	1081	CAGCCCGCCCTCCACTGCCACCGACTGTAGGGCTGCCCCAGCCCCAGGACTGCC *****
P_AAX80056	1081	CAGCCCGCCCTCCACTGCCACCGACTGTAGGGCTGCCCCAGCCCCAGGACTGCC
DNA44804	1141	ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG *****
P_AAX80056	1141	ACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG

BLAST RESULTS A-9

DNA44804	1201	CTTGTCCCCGAAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG *****
P_AAX80056	1201	CTTGTCCCCGAAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG *****
DNA44804	1261	GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCCTGGGCATCGAGCC *****
P_AAX80056	1261	GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCCTGGGCATCGAGCC *****
DNA44804	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCA *****
P_AAX80056	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCA *****
DNA44804	1381	GCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGATAAGCGGCTGGTGAC *****
P_AAX80056	1381	GCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGATAAGCGGCTGGTGAC *****
DNA44804	1441	GCTGCGACTGCCTGCCTCGCTGAGTACACGGTACCCAGCTGCGGCCAACGCCAC *****
P_AAX80056	1441	GCTGCGACTGCCTGCCTCGCTGAGTACACGGTACCCAGCTGCGGCCAACGCCAC *****
DNA44804	1501	TTACTCCGTCTGTGTCATGCCTTGGGCCGGCGGGTGCCGGAGGGCGAGGAGGCCCTG *****
P_AAX80056	1501	TTACTCCGTCTGTGTCATGCCTTGGGCCGGCGGGTGCCGGAGGGCGAGGAGGCCCTG *****
DNA44804	1561	CGGGGAGGCCATACACCCCCAGCCGTCACTCCAACCACGCCCCAGTCACCCAGGCCCG *****
P_AAX80056	1561	CGGGGAGGCCATACACCCCCAGCCGTCACTCCAACCACGCCCCAGTCACCCAGGCCCG *****
DNA44804	1621	CGAGGGCAACCTGCCGTCCCTCATGGCCCGCCCTGGCGCGGTGCTCCTGGCGCGCT *****
P_AAX80056	1621	CGAGGGCAACCTGCCGTCCCTCATGGCCCGCCCTGGCGCGGTGCTCCTGGCGCGCT *****
DNA44804	1681	GGCTCGGGTGGGGCAGCCTACTGTGTGCCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA *****
P_AAX80056	1681	GGCTCGGGTGGGGCAGCCTACTGTGTGCCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA *****
DNA44804	1741	GGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAGGGAGTGAAGGTCCC *****
P_AAX80056	1741	GGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAGGGAGTGAAGGTCCC *****
DNA44804	1801	CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGTGGAGAGGCCCTGCCAGCGGGTCTGA *****
P_AAX80056	1801	CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGTGGAGAGGCCCTGCCAGCGGGTCTGA *****
DNA44804	1861	GTGTGAGGTGCCACTCATGGGCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA *****
P_AAX80056	1861	GTGTGAGGTGCCACTCATGGGCTCCAGGGCCTGGCCTCCAGTCACCCCTCACGCAA *****
DNA44804	1921	GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA *****
P_AAX80056	1921	GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA *****
DNA44804	1981	TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCAAACCTCGGGGATGTG *****
P_AAX80056	1981	TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCAAACCTCGGGGATGTG *****

BLAST RESULTS A-10

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DNA44804 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
*****
P_AAX80056 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

DNA44804 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGGCCCTAACGTCCCCAGAACCGAGTGCCTATG
*****
P_AAX80056 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGGCCCTAACGTCCCCAGAACCGAGTGCCTATG

DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA
*****
P_AAX80056 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA

DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGCTCTCCACTCCAGGCAGGACCCCTGGGG
*****
P_AAX80056 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGCTCTCCACTCCAGGCAGGACCCCTGGGG

DNA44804 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCAGGCTGTGTGACTC
*****
P_AAX80056 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCAGGCTGTGTGACTC

DNA44804 2341 TAGTCTGGCCCCAGGAAGCGAAGGAACAAAAGAAAATGGAAAGAGATGCTTTAGGAA
*****
P_AAX80056 2341 TAGTCTGGCCCCAGGAAGCGAAGGAACAAAAGAAAATGGAAAGAGATGCTTTAGGAA

DNA44804 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG
*****
P_AAX80056 2401 CATGTTTGCTTTTAAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG

DNA44804 2461 GGAAGATGTTTCAAACCTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATA
*****
P_AAX80056 2461 GGAAGATGTTTCAAACCTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATA

DNA44804 2521 TGAAGGCCTTGTAAAGAAAAATAAAAAAAAAAAA
*****
P_AAX80056 2521 TGAAGGCCTTGTAAAGAAAAATAAAAAAAAAAAA

>4 P_AAX87261 cDNA clone encoding human PRO357, amplified in tumour cells. (2555
bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

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DNA44804	1	GGGGCGGGTGGACCGGACTCGAACGCAGTGCTCGGGACCCAGGACCCCCCTGGGCC
P_AAX87261	1	GGGGCGGGTGGACCGGACTCGAACGCAGTGCTCGGGACCCAGGACCCCCCTGGGCC
DNA44804	61	GACCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCGGCCGCTCCCTGCGCCGCC
P_AAX87261	61	GACCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCGGCCGCTCCCTGCGCCGCC
DNA44804	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
P_AAX87261	121	CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACT
DNA44804	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGAC
P_AAX87261	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGAC

BLAST RESULTS A-11

DNA44804	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT *****
P_AAX87261	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT *****
DNA44804	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCT *****
P_AAX87261	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCT *****
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAACAGATCGCCAGCCTGCGCCTGCCCG *****
P_AAX87261	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAACAGATCGCCAGCCTGCGCCTGCCCG *****
DNA44804	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCAGCATCCTGGA *****
P_AAX87261	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCAGCATCCTGGA *****
DNA44804	481	CACTGCCAACGTGGAGGCCTGCAGCTGGCTGGCTGGATGTGTCGACAGCAGCTGGACGAGGG *****
P_AAX87261	481	CACTGCCAACGTGGAGGCCTGCAGCTGGCTGGATGTGTCGACAGCAGCTGGACGAGGG *****
DNA44804	541	GCTCTCAGCCGCTTGCAGAACCTCCACGACCTGGATGTGTCGACAGCAGCTGGAGCG *****
P_AAX87261	541	GCTCTCAGCCGCTTGCAGAACCTCCACGACCTGGATGTGTCGACAGCAGCTGGAGCG *****
DNA44804	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCGGCTGGCCGGCAACAC *****
P_AAX87261	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCGGCTGGCCGGCAACAC *****
DNA44804	661	CCGCATTGCCAGCTGCAGCCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA *****
P_AAX87261	661	CCGCATTGCCAGCTGCAGCCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGA *****
DNA44804	721	TGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCT *****
P_AAX87261	721	TGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCT *****
DNA44804	781	GCGGCTGCTGGCAGCTGCCGCCAACCCCTTAACACTGCGTGTGCCCCCTGAGCTGGTTGG *****
P_AAX87261	781	GCGGCTGCTGGCAGCTGCCGCCAACCCCTTAACACTGCGTGTGCCCCCTGAGCTGGTTGG *****
DNA44804	841	CCCCTGGGTGCGAGAGGCCACGTCACACTGCCAGCCCTGAGGAGACGCGCTGCCACTT *****
P_AAX87261	841	CCCCTGGGTGCGAGAGGCCACGTCACACTGCCAGCCCTGAGGAGACGCGCTGCCACTT *****
DNA44804	901	CCCGCCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGAACAGCCGACTTGGCTGCC *****
P_AAX87261	901	CCCGCCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGAACAGCCGACTTGGCTGCC *****
DNA44804	961	AGCCACCACCAACCACAGCCACAGTGCCCACACAGGAGGCCGTGGTGGAGCCACAGC *****
P_AAX87261	961	AGCCACCACCAACCACAGCCACAGTGCCCACACAGGAGGCCGTGGTGGAGCCACAGC *****
DNA44804	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCC *****
P_AAX87261	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCC *****
DNA44804	1081	CAGCCCGCCCTCCACTGCCAACGACTGTAGGGCTGTCCCCCAGCCCCAGGACTGCC *****

BLAST RESULTS A-12

P_AAX87261 1081 CAGCCCGCCCTCCACTGCCCAACGGACTGTAGGGCCTGCCCCAGCCCCAGGACTGCC
DNA44804 1141 ACCGTCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG
P_AAX87261 1141 ACCGTCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGGCACCACCTGGCGTG
DNA44804 1201 CTTGTCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG
P_AAX87261 1201 CTTGTCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATGGGCAGGGGACACG
DNA44804 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCCTGGGCATCGAGCC
P_AAX87261 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCCTGGGCATCGAGCC
DNA44804 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCAGGGGAGCTCCGTGCA
P_AAX87261 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGTACCTCAGGGGAGCTCCGTGCA
DNA44804 1381 GCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
P_AAX87261 1381 GCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
DNA44804 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCAGCTGCGGCCAACGCCAC
P_AAX87261 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCAGCTGCGGCCAACGCCAC
DNA44804 1501 TTACTCCGTCTGTTCATGCCATTGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
P_AAX87261 1501 TTACTCCGTCTGTTCATGCCATTGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
DNA44804 1561 CGGGGAGGCCATACACCCCCAGCCGTCACTCAAACACGCCAGTCACCCAGGCCCG
P_AAX87261 1561 CGGGGAGGCCATACACCCCCAGCCGTCACTCAAACACGCCAGTCACCCAGGCCCG
DNA44804 1621 CGAGGGCAACCTGCCGCTCCTCATTCGCCCCGCCCTGGCCGCGGTGCTCTGGCGCGCT
P_AAX87261 1621 CGAGGGCAACCTGCCGCTCCTCATTCGCCCCGCCCTGGCCGCGGTGCTCTGGCGCGCT
DNA44804 1681 GGCTCGGTGGGGCAGCCTACTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
P_AAX87261 1681 GGCTCGGTGGGGCAGCCTACTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
DNA44804 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCC
P_AAX87261 1741 GGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCC
DNA44804 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGCTGA
P_AAX87261 1801 CTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGCTGA
DNA44804 1861 GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA
P_AAX87261 1861 GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA
DNA44804 1921 GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA
P_AAX87261 1921 GCCCTACATCTAACGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGA

P_AAX87261 1921 GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGCGGGCTCTCAGCCAGTGAGA
 DNA44804 1981 TGGCCAGCCCCCTCTGCTGCCACACCACGTAAAGTCTCAGTCCCAACCTCGGGGATGTG

 P_AAX87261 1981 TGGCCAGCCCCCTCTGCTGCCACACCACGTAAAGTCTCAGTCCCAACCTCGGGGATGTG
 DNA44804 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

 P_AAX87261 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
 DNA44804 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG

 P_AAX87261 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
 DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA

 P_AAX87261 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCACGGCGGGCCCTGCCA
 DNA44804 2221 TGTGCTGGTAACGCATGCCTGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG

 P_AAX87261 2221 TGTGCTGGTAACGCATGCCTGGCCCTGCTGGCTCTCCACTCCAGGCGGACCCCTGGGG
 DNA44804 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC

 P_AAX87261 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
 DNA44804 2341 TAGTCTTGGCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGGAA

 P_AAX87261 2341 TAGTCTTGGCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGGAA
 DNA44804 2401 CATGTTTGCTTTTAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG

 P_AAX87261 2401 CATGTTTGCTTTTAAATATATATATTTATAAGAGATCCTTCCCATTATTCTG
 DNA44804 2461 GGAAGATTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATA

 P_AAX87261 2461 GGAAGATTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATA
 DNA44804 2521 TGAAGGCCTTTGTAAGAAAAAATAAAAAAAAAAA

 P_AAX87261 2521 TGAAGGCCTTTGTAAGAAAAAATAAAAAAAAAAA
 >5 P_AAA58765 cDNA encoding a leucine-rich surface glycoprotein (LRSG). (2852
 bp) [2 segs]
 Score = 2142 (4246 bits), Expect = 0.0 [P_AAA58765, seg 1/2]
 Identities = 2142/2142 (100%), at 407, 655-2548, 2796, Strand +/-
 DNA44804 407 CTGCGCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCTCCTGGCCCTGGAG

 P_AAA58765 655 CTGCGCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCTCCTGGCCCTGGAG
 DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG

 P_AAA58765 715 CCCGGCATCCTGGACACTGCCAACGTGGAGGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG
 DNA44804 527 CAGCTGGACGAGGGCTTTCAGCCGCTTGGCAACCTCCACGACCTGGATGTGTCCGAC

BLAST RESULTS A-14

P_AAA58765 775 CAGCTGGACGAGGGGCTTTCAGCCGTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
DNA44804 587 AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCGCCTGC

P_AAA58765 835 AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCGCCTGC
DNA44804 647 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCTGGCTGCC

P_AAA58765 895 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCTGGCTGCC
DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAACGCCTGCAGGCCCTGCCTGGCGACCTCTCG

P_AAA58765 955 CTGCAGGAGCTGGATGTGAGCAACCTAACGCCTGCAGGCCCTGCCTGGCGACCTCTCG
DNA44804 767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCC

P_AAA58765 1015 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCC
DNA44804 827 CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGGCCAGGAG

P_AAA58765 1075 CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGGCCAGGAG
DNA44804 887 ACGCGCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGACTACGCC

P_AAA58765 1135 ACGCGCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804 947 GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACCACAGGCCCCGTGGT

P_AAA58765 1195 GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACCACAGGCCCCGTGGT
DNA44804 1007 CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCC

P_AAA58765 1255 CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCC
DNA44804 1067 GCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG

P_AAA58765 1315 GCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG
DNA44804 1127 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG

P_AAA58765 1375 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG
DNA44804 1187 CACCACCTGGCGTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG

P_AAA58765 1435 CACCACCTGGCGTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG
DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCACGGTCCCTGACC

P_AAA58765 1495 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCACGGTCCCTGACC
DNA44804 1307 CTGGGCATCGAGCCGGTGAGCCCACCTCCCTGCGCTGGGCTGCAGCGCTACCTCCAG

P_AAA58765 1555 CTGGGCATCGAGCCGGTGAGCCCACCTCCCTGCGCTGGGCTGCAGCGCTACCTCCAG
DNA44804 1367 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGGGCCCTGAT

P_AAA58765 1615 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGGGCCCTGAT

Blast results A-16

DNA44804	1427	AAGCGGCTGGTGACCGCTGCGACTGCCTGCCCGCTCGCTGAGTACACGGTCACCCAGCTG *****
P_AAA58765	1675	AAGCGGCTGGTGACCGCTGCGACTGCCTGCCCGCTCGCTGAGTACACGGTCACCCAGCTG *****
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCCCGGCGGGTGCCGGAG *****
P_AAA58765	1735	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCCCGGCGGGTGCCGGAG *****
DNA44804	1547	GGCGAGGAGGCCTGCCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA *****
P_AAA58765	1795	GGCGAGGAGGCCTGCCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA *****
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCGCCCTGGCCGCGGTG *****
P_AAA58765	1855	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCGCCCTGGCCGCGGTG *****
DNA44804	1667	CTCCTGGCCCGCGCTGGCTGCCGTGGGAGGCCAGCCTACTGTGTGCGGGGGCGGGCATG *****
P_AAA58765	1915	CTCCTGGCCCGCGCTGGCTGCCGTGGGAGGCCAGCCTACTGTGTGCGGGGGCGGGCATG *****
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG *****
P_AAA58765	1975	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG *****
DNA44804	1787	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG *****
P_AAA58765	2035	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG *****
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCTGGCCTCCAGTCA *****
P_AAA58765	2095	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCTGGCCTCCAGTCA *****
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
P_AAA58765	2155	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCC *****
P_AAA58765	2215	CTCAGCCAGTGAGATGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCC *****
DNA44804	2027	ACCTCGGGGATGTGTCAGACAGGGCTGTGACCAAGCTGGGCCCTGTTCCCTCTGGA *****
P_AAA58765	2275	ACCTCGGGGATGTGTCAGACAGGGCTGTGACCAAGCTGGGCCCTGTTCCCTCTGGA *****
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
P_AAA58765	2335	CCTCGGTCTCCTCATCTGTGAGATGCTGTGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
DNA44804	2147	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGGCAC *****
P_AAA58765	2395	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGGCAC *****
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****
P_AAA58765	2455	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****

Blast results A-IV

DNA44804 2267 GCGGGACCTGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

P AAA58765 2515 GCGGGACCTGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

DNA44804 2327 CGGCTGTGTGACTCTAGTCTGGCCCCAGGAAGCGAACAAAGAAAATGGAAAGGA

P AAA58765 2575 CGGCTGTGTGACTCTAGTCTGGCCCCAGGAAGCGAACAAAGAAAATGGAAAGGA

DNA44804 2387 AGATGCTTAGAACATGTTTGCTTTAAAATATATATATTTATAAGAGATCCTT

P AAA58765 2635 AGATGCTTAGAACATGTTTGCTTTAAAATATATATATTTATAAGAGATCCTT

DNA44804 2447 TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA

P AAA58765 2695 TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA

DNA44804 2507 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA

P AAA58765 2755 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA

Score = 406 (805 bits), Expect = 0.0 [P AAA58765, seg 2/2]
Identities = 409/410 (99%), at 1,24-410,433, Strand +/+

DNA44804 1 GGGGCGGGTGGACCGGACTCGAACGCAGTGCTTCGGGACCCAGGACCCCTCGGGCCC

P AAA58765 24 GGGGCGGGTGGACCGGACTCGAACGCAGTGCTTCGGGACCCAGGACCCCTCGGGCCC

DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGGCCGGCTCCCTGCGCCGCCGCG

P AAA58765 84 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGGCCGGCTCCCTGCGCCGCCGCG

DNA44804 121 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

P AAA58765 144 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

DNA44804 181 GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGAC

P AAA58765 204 GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGAC

DNA44804 241 AGTCTCTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

P AAA58765 264 AGTCTCTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

DNA44804 301 GGGGCTGTACGTCTTGAGAACGGCATCACCAGTGCACGCAAGCAGCTTGCCGGCCT

P AAA58765 324 GGGGCTGTACGTCTTGAGAACGGCATCACCAGTGCACGCAAGCAGCTTGCCGGCCT

DNA44804 361 GCCGGGCCTGCAGCTCTGGACCTGTCACAGAACAGATGCCAGCCTGC

P AAA58765 384 GCCGGGCCTGCAGCTCTGGACCTGTCACAGAACAGATGCCAGCCTGC

>6 AC012676 Homo sapiens chromosome 16 clone RP11-295D4, WORKING DRAFT (172139 bp) [3 segs]

Score = 2138 (4238 bits), Expect = 0.0 [AC012676, seg 1/3]
Identities = 2141/2142 (99%), at 407,81365-2548,83506, Strand +/+

DNA44804 407 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGGCCAACAGCCTCTGGCCCTGGAG

BLAST RESULTS A-17

AC012676	81365	***** CTGCGCCTGCCCGCCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
DNA44804	467	***** CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG
AC012676	81425	***** CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG
DNA44804	527	***** CAGCTGGACGAGGGCTCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC
AC012676	81485	***** CAGCTGGACGAGGGCTCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC
DNA44804	587	***** AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCGCCTGCG
AC012676	81545	***** AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCGCCTGCG
DNA44804	647	***** CTGGCCGGAAACACCCGATTGCCAGCTGCGGCCCAGGACCTGCCGGCCTGGCTGCC
AC012676	81605	***** CTGGCCGGAAACACCCGATTGCCAGCTGCGGCCCAGGACCTGCCGGCCTGGCTGCC
DNA44804	707	***** CTGCAGGAGCTGGATGTGAGAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTGGGC
AC012676	81665	***** CTGCAGGAGCTGGATGTGAGAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTGGGC
DNA44804	767	***** CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCAGCAACCCCTTAACACTGCGTGTGCC
AC012676	81725	***** CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCAGCAACCCCTTAACACTGCGTGTGCC
DNA44804	827	***** CTGAGCTGGTTGGCCCTGGGTGCGGAGAGCACGTCACACTGCCAGGCCCTGAGGAG
AC012676	81785	***** CTGAGCTGGTTGGCCCTGGGTGCGGAGAGCACGTCACACTGCCAGGCCCTGAGGAG
DNA44804	887	***** ACGCGCTGCCACTTCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
AC012676	81845	***** ACGCGCTGCCACTTCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804	947	***** GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACCCACAGGCCCCGTGGTG
AC012676	81905	***** GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACCCACAGGAGGCCCCGTGGTG
DNA44804	1007	***** CGGGAGCCCACAGCCTTGTCTCTAGCTTGCTCCTACCTGGCTTAGCCCCACAGCGCCG
AC012676	81965	***** CGGGAGCCCACAGCCTTGTCTCTAGCTTGCTCCTACCTGGCTTAGCCCCACAGAGCCG
DNA44804	1067	***** GCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCTGTCCCCCAG
AC012676	82025	***** GCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCTGTCCCCCAG
DNA44804	1127	***** CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG
AC012676	82085	***** CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG
DNA44804	1187	***** CACCACCTGGCGTGTGGCTTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG
AC012676	82145	***** CACCACCTGGCGTGTGGCTTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG
DNA44804	1247	***** GGGCAGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCCCTGACC

Blast results A-16

AC012676	82205	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG *****
AC012676	82265	CTGGGCATCGAGCCGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT *****
AC012676	82325	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG *****
AC012676	82385	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCTTGGGGCCCGGGCGGGTGCCGGAG *****
AC012676	82445	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCTTGGGGCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA *****
AC012676	82505	GGCGAGGAGGCCTGCGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTCGCCTGGCCCGGGTG *****
AC012676	82565	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTCGCCTGGCCCGGGTG
DNA44804	1667	CTCCTGGCCCGCCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGGGGCGGCCATG *****
AC012676	82625	CTCCTGGCCCGCCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGGGGCGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG *****
AC012676	82685	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGGGTGGAGAGGCCCTG *****
AC012676	82745	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGCCTCCAGTCA *****
AC012676	82805	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGCCTCCAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGCT *****
AC012676	82865	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGCT
DNA44804	1967	CTCAGCCAGTGAGATGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA *****
AC012676	82925	CTCAGCCAGTGAGATGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGCGAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA *****
AC012676	82985	ACCTCGGGGATGTGCGAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
AC012676	83045	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA

BLAST RESULTS - 19

DNA44804	2147	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCAC *****
AC012676	83105	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCTGGCAC
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****
AC012676	83165	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA
DNA44804	2267	GGCGGACCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGG *****
AC012676	83225	GGCGGACCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804	2327	C GGCTGTGACTCTAGTCTTGGCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA *****
AC012676	83285	C GGCTGTGACTCTAGTCTTGGCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA
DNA44804	2387	AGATGCTTTAGGAACATGTTTGCTTTAAAATATATATATTTATAAGAGATCCTT *****
AC012676	83345	AGATGCTTTAGGAACATGTTTGCTTTAAAATATATATATTTATAAGAGATCCTT
DNA44804	2447	TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGAA *****
AC012676	83405	TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGAA
DNA44804	2507	GACAAACGATGATATGAAGGCCTTGTAAAGAAAAATAAAA *****
AC012676	83465	GACAAACGATGATATGAAGGCCTTGTAAAGAAAAATAAAA

Score = 280 (555 bits), Expect = e-154 [AC012676, seg 2/3]

Identities = 283/284 (99%), at 127,80860-410,81143, Strand +/-

DNA44804	127	GGGACAGAAGATGTGCTCCAGGGCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT *****
AC012676	80860	GGGACAGAAGATGTGCTCCAGGGCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
DNA44804	187	GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT *****
AC012676	80920	GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT
DNA44804	247	CTGCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCT *****
AC012676	80980	CTGCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCT
DNA44804	307	GTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCTGCCGG *****
AC012676	81040	GTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCCTGCCGG
DNA44804	367	CCTGCAGCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGC *****
AC012676	81100	CCTGCAGCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGC

Score = 128 (254 bits), Expect = 1e-63 [AC012676, seg 3/3]

Identities = 128/128 (100%), at 1,71859-128,71986, Strand +/-

DNA44804	1	GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTCGGACCCAGGACCCCTCGGGCCC *****
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BLAST RESULTS A-20

AC012676 71859 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTGGGCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGCC

AC012676 71919 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGCC
DNA44804 121 CCTCCCGG

AC012676 71979 CCTCCCGG

>7 AC005222 Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete
(40619 bp) [3 segs]
Score = 2138 (4238 bits), Expect = 0.0 [AC005222, seg 1/3]
Identities = 2141/2142 (99%), at 407,22755-2548,24896, Strand +/-

DNA44804 407 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

AC005222 22755 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG

AC005222 22815 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG

DNA44804 527 CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC

AC005222 22875 CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC

DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCCCTGCGG

AC005222 22935 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCCCTGCGG

DNA44804 647 CTGGCCGGCAACACCCGATTGCCAGCTGCCAGCTGGCCGGGCTGGCTGGCTGCC

AC005222 22995 CTGGCCGGCAACACCCGATTGCCAGCTGCCAGCTGGCCGGGCTGGCTGGCTGCC

DNA44804 707 CTGCAGGAGCTGGATGTGAGCAAACCTAAGCCTGCAAGGCCCTGCCAGCTGGCGACCTCTCGGGC

AC005222 23055 CTGCAGGAGCTGGATGTGAGCAAACCTAAGCCTGCAAGGCCCTGCCAGCTGGCGACCTCTCGGGC

DNA44804 767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTAACCTGGCTGTGCCCC

AC005222 23115 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTAACCTGGCTGTGCCCC

DNA44804 827 CTGAGCTGGTTGGCCCTGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

AC005222 23175 CTGAGCTGGTTGGCCCTGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

DNA44804 887 ACGCCTGCCACTTCCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

AC005222 23235 ACGCCTGCCACTTCCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

DNA44804 947 GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCCACCCAGGAGCCCGTGGT

AC005222 23295 GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCCACCCAGGAGCCCGTGGT

DNA44804 1007 CGGGAGCCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCCG

BLAST RESULTS A-21

AC005222	23355	CGGGAGCCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGAGCCG
DNA44804	1067	GCCACTGAGGCCCGAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG
AC005222	23415	***** GCCACTGAGGCCCGAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGGACACGG
AC005222	23475	***** CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGGACACGG
DNA44804	1187	CACCACCTGGCGTGTTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG
AC005222	23535	***** CACCACCTGGCGTGTTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
AC005222	23595	***** GGGCAGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCACCTCCCTGCGCGTGGGCTGCAGCGCTACCTCCAG
AC005222	23655	***** CTGGGCATCGAGCCGGTGAGCCCACCTCCCTGCGCGTGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATGGGCCCTGAT
AC005222	23715	***** GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTACCCAGCTG
AC005222	23775	***** AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTACCCAGCTG
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTCATGCCTTGGGCCGGGGTGGAG
AC005222	23835	***** CGGCCAACGCCACTTACTCCGTCTGTGTCATGCCTTGGGCCGGGGTGGAG
DNA44804	1547	GGCGAGGAGGCCTGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
AC005222	23895	***** GGCGAGGAGGCCTGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
DNA44804	1607	GTCACCCAGGCCCGAGGGCAACCTGCCGCTCCTCATGCGCCGCCCTGGCGCGGTG
AC005222	23955	***** GTCACCCAGGCCCGAGGGCAACCTGCCGCTCCTCATGCGCCGCCCTGGCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGTGGGGCAGCCTACTGTGTGCGGGGGGGGGCATG
AC005222	24015	***** CTCCTGGCCGCGCTGGCTGCGTGGGGCAGCCTACTGTGTGCGGGGGGGGGCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACTGGAG
AC005222	24075	***** GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
AC005222	24135	***** GGAGTGAAGGTCCCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
AC005222	24195	***** CCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

BLAST RESULTS A-2Z

DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
AC005222	24255	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCA *****
AC005222	24315	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCA *****
DNA44804	2027	ACCTCGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGCCCTGTTCCCTCTGGA *****
AC005222	24375	ACCTCGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGCCCTGTTCCCTCTGGA *****
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
AC005222	24435	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
DNA44804	2147	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAAACGTGCAGTCCCTGGGCAC *****
AC005222	24495	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAAACGTGCAGTCCCTGGGCAC *****
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCA *****
AC005222	24555	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCA *****
DNA44804	2267	GGCGGACCCCTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG *****
AC005222	24615	GGCGGACCCCTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG *****
DNA44804	2327	CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGAAAGGA *****
AC005222	24675	CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGAAAGGA *****
DNA44804	2387	AGATGCTTTAGGAACATGTTTGCTTTAAAATATATATATTATAAGAGATCCTT *****
AC005222	24735	AGATGCTTTAGGAACATGTTTGCTTTAAAATATATATATTATAAGAGATCCTT *****
DNA44804	2447	TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA *****
AC005222	24795	TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA *****
DNA44804	2507	GACAAACGATGATATGAAGGCCTTGTAAAGAAAAATAAAA *****
AC005222	24855	GACAAACGATGATATGAAGGCCTTGTAAAGAAAAATAAAA *****
Score = 280 (555 bits), Expect = e-154 [AC005222, seg 2/3] Identities = 283/284 (99%), at 127,22250-410,22533, Strand +/-		
DNA44804	127	GGGACAGAAGATGTGCTCCAGGGCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT *****
AC005222	22250	GGGACAGAAGATGTGCTCCAGGGCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT *****
DNA44804	187	GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT *****
AC005222	22310	GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT *****
DNA44804	247	CTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCT *****

Blast results A-23

AC005222 22370 CTGCACTGCCGCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCT
DNA44804 307 GTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCTGCCGGG

AC005222 22430 GTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCTGCCGGG
DNA44804 367 CCTGCAGCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGC

AC005222 22490 CCTGCAGCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGC

Score = 128 (254 bits), Expect = 1e-63 [AC005222, seg 3/3]
Identities = 128/128 (100%), at 1,13249-128,13376, Strand +/

DNA44804 1 GGGGCGGGTGGACCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCC

AC005222 13249 GGGGCGGGTGGACCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGG

AC005222 13309 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGG

DNA44804 121 CCTCCCGG

AC005222 13369 CCTCCCGG

>8 P_AAF44105 Human PRO1282 (UNQ652) nucleotide sequence SEQ ID NO:51. (2768 bp)
[2 segs]
Score = 2127 (4216 bits), Expect = 0.0 [P_AAF44105, seg 1/2]
Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand
+/

DNA44804 407 CTGCGCCTGCCGCCCTGCTGCTGGACCTCAGCCACAACAGCCTCTGGCCCTGGAG

P_AAF44105 615 CTGCGCCTGCCGCCCTGCTGCTGGACCTCAGCCACAACAGCCTCTGGCCCTGGAG
DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGCTGGAG

P_AAF44105 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGCTGGAG
DNA44804 527 CAGCTGGACGAGGGCTTCAAGCCGCTTGCACGACCTGGATGTGTCGAC

P_AAF44105 735 CAGCTGGACGAGGGCTTCAAGCCGCTTGCACGACCTGGATGTGTCGAC
DNA44804 587 AACCAAGCTGGAGCGAGTGCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCGG

P_AAF44105 795 AACCAAGCTGGAGCGAGTGCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCGG
DNA44804 647 CTGGCCGGCAACACCCGATTGCCAGCTGCGGCCGAGGACCTGGCCGGCTGGCTGCC

P_AAF44105 855 CTGGCCGGCAACACCCGATTGCCAGCTGCGGCCGAGGACCTGGCCGGCTGGCTGCC
DNA44804 707 CTGCAGGAGCTGGATGTGAGAACCTAAGCCTGCAGGCCCTGCCGGCGACCTCTCGGGC

P_AAF44105 915 CTGCAGGAGCTGGATGTGAGAACCTAAGCCTGCAGGCCCTGCCGGCGACCTCTCGGGC
DNA44804 767 CTCTTCCCCGCCCTGCGGCTGCTGGCAGCTGCCGAAACCCCTCAACTGCGTGTGCC

Blast results A-24

P_AAF44105	975	***** CTCTTCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCC *****
DNA44804	827	CTGAGCTGGTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGCCCTGAGGAG *****
P_AAF44105	1035	CTGAGCTGGTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGCCCTGAGGAG *****
DNA44804	887	ACCGCGCTGCCACTTCCC GCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC *****
P_AAF44105	1095	ACCGCGCTGCCACTTCCC GCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC *****
DNA44804	947	GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGGCCACCACAGGCCCCGTGGTG *****
P_AAF44105	1155	GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGGCCACCACAGGCCCCGTGGTG *****
DNA44804	1007	CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG *****
P_AAF44105	1215	CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG *****
DNA44804	1067	GCCACTGAGGCCAGCCGGCCCTCCACTGCCCCACCGACTGTAGGGCCTGCCCCAG *****
P_AAF44105	1275	GCCACTGAGGCCAGCCGGCCCTCCACTGCCCCACCGACTGTAGGGCCTGCCCCAG *****
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG *****
P_AAF44105	1335	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG *****
DNA44804	1187	CACCACCTGGCGTGTGGCTTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG *****
P_AAF44105	1395	CACCACCTGGCGTGTGGCTTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG *****
DNA44804	1247	GGGCAGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCCCTGACC *****
P_AAF44105	1455	GGGCAGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCCCTGACC *****
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGCTACCTCCAG *****
P_AAF44105	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGCTGCAGCGCTACCTCCAG *****
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGGGCCCTGAT *****
P_AAF44105	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATGGGCCCTGAT *****
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCCTGCCCTCGCTGAGTACACGGTCACCCAGCTG *****
P_AAF44105	1635	AAGCGGCTGGTGACGCTGCGACTGCCCTGCCCTCGCTGAGTACACGGTCACCCAGCTG *****
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCGGGGTGCAGGAG *****
P_AAF44105	1695	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCGGGGTGCAGGAG *****
DNA44804	1547	GGCGAGGAGGCCCTGCGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCAACGCC *****
P_AAF44105	1755	GGCGAGGAGGCCCTGCGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCAACGCC *****
DNA44804	1607	GTCACCCAGGCCGCGAGGGCAACCTGCCGCTCCTCATGGCCCCGCCCTGGCGCGGTG *****

BLAST RESULTS A-26

P_AAF44105 1815 GTCACCCAGGCCCGCGAGGGCAACCTGCCCTCCTCATTCGCCCCCCTGGCCCGGTG
DNA44804 1667 CTCCTGGCCGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGGGGGCCATG

P_AAF44105 1875 CTCCTGGCCGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGGGGGCCATG
DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG

P_AAF44105 1935 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACTGGAG
DNA44804 1787 GGAGTGAAGGTCCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AAF44105 1995 GGAGTGAAGGTCCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804 1847 CCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCTCCAGTCA

P_AAF44105 2055 CCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCTCCAGTCA
DNA44804 1907 CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT

P_AAF44105 2115 CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT
DNA44804 1967 CTCAGCCAGTGAGATGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCA

P_AAF44105 2175 CTCAGCCAGTGAGATGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCA
DNA44804 2027 ACCTCGGGATGTGTGCAGACAGGGCTGTGACCACAGCTGGCCCTGTTCCCTCTGGA

P_AAF44105 2235 ACCTCGGGATGTGTGCAGACAGGGCTGTGACCACAGCTGGCCCTGTTCCCTCTGGA
DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA

P_AAF44105 2295 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGCAC

P_AAF44105 2355 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGCAC
DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCA

P_AAF44105 2415 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCCCTGCTGGCTCTCCACTCCA
DNA44804 2267 GGCGGGACCCCTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG

P_AAF44105 2475 GGCGGGACCCCTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGACTCTAGTCTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA

P_AAF44105 2535 CGGCTGTGACTCTAGTCTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA
DNA44804 2387 AGATGCTTACGGAAACATGTTGCTTTAAATATATATATATTATAAGAGATCCTT

P_AAF44105 2595 AGATGCTTACGGAAACATGTTGCTTTAA--ATATATATATTATAAGAGATCCTT
DNA44804 2447 TCCCATTATTCTGGAAAGATGTTTCAAACACTCAGAGACAAGGACTTGGTTTGAA

P_AAF44105 2653 TCCCATTATTCTGGAAAGATGTTTCAAACACTCAGAGACAAGGACTTGGTTTGAA

BLAST RESULTS A-24

DNA44804 2507 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAATAAAA

P_AAF44105 2713 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [P_AAF44105, seg 2/2]
Identities = 392/393 (99%), at 18,1-410,393, Strand +/-

DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCGACCCGCCAGGAAAGAC

P_AAF44105 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCGACCCGCCAGGAAAGAC

DNA44804 78 TGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA

P_AAF44105 61 TGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA

DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGG

P_AAF44105 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGG

DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAAGCCAGCACAGCAGTCTTCTGCACTGCC

P_AAF44105 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAAGCCAGCACAGCAGTCTTCTGCACTGCC

DNA44804 258 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTG

P_AAF44105 241 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTG

DNA44804 318 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGGCTGCCGGGCTGCAGCTCC

P_AAF44105 301 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGGCTGCCGGGCTGCAGCTCC

DNA44804 378 TGGACCTGTCACAGAACAGATGCCAGCCTGC

P_AAF44105 361 TGGACCTGTCACAGAACAGATGCCAGCCTGC

>9 P_AAF92065 Human PRO1282 cDNA. (2768 bp) [2 segs]
Score = 2127 (4216 bits), Expect = 0.0 [P_AAF92065, seg 1/2]
Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand +/-

DNA44804 407 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

P_AAF92065 615 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCCGGCTGGCTGGTCTGGGCTGCAG

P_AAF92065 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCCGGCTGGCTGGTCTGGGCTGCAG

DNA44804 527 CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGAC

P_AAF92065 735 CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGAC

DNA44804 587 AACCCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCCCTGC

P_AAF92065 795 AACCCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCTGACGCCCTGC

Blast results A-27

DNA44804	647	CTGGCCGGCAACACCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGCTGCC *****
P_AAF92065	855	CTGGCCGGCAACACCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGCTGCC *****
DNA44804	707	CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGC *****
P_AAF92065	915	CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTCGGGC *****
DNA44804	767	CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCC *****
P_AAF92065	975	CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCC *****
DNA44804	827	CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGGCCGTGAGGAG *****
P_AAF92065	1035	CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGGCCGTGAGGAG *****
DNA44804	887	ACCGCGCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGACTACGCC *****
P_AAF92065	1095	ACCGCGCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTGACTACGCC *****
DNA44804	947	GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCACCACAGGCGGTGGTG *****
P_AAF92065	1155	GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCACCACAGGCGGTGGTG *****
DNA44804	1007	CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG *****
P_AAF92065	1215	CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG *****
DNA44804	1067	GCCACTGAGGCCAGCCGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG *****
P_AAF92065	1275	GCCACTGAGGCCAGCCGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG *****
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG *****
P_AAF92065	1335	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG *****
DNA44804	1187	CACCACCTGGCGTGTGGCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG *****
P_AAF92065	1395	CACCACCTGGCGTGTGGCCGAAGGCTTCACGGGCTGTACTGTGAGAGCCAGATG *****
DNA44804	1247	GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCCCTGACC *****
P_AAF92065	1455	GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCCCTGACC *****
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCTGGGCTGCAGCGCTACCTCCAG *****
P_AAF92065	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCTGGGCTGCAGCGCTACCTCCAG *****
DNA44804	1367	GGGAGCTCGTGCAGCTCAGGAGCCTCGTCTCACCTATCGAACCTATCGGGCCTGAT *****
P_AAF92065	1575	GGGAGCTCGTGCAGCTCAGGAGCCTCGTCTCACCTATCGAACCTATCGGGCCTGAT *****
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG *****
P_AAF92065	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG *****
DNA44804	1487	CGGCCAACGCCACTTACTCCGTGTGTCATGCCCTTGGGCCGGCGGGTGCCGGAG *****

BLAST RESULTS A-28

P_AAF92065 1695 CGGCCAACGCCACTTACTCCGTCTGTGTATGCCATTGGGCCCCGGCGGGAG
DNA44804 1547 GGCGAGGAGGCCTGCAGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
P_AAF92065 1755 GGCGAGGAGGCCTGCAGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
DNA44804 1607 GTCACCCAGGCCCGCGAGGGCAACCTGCCCTCATTGCGCCCGCCCTGGCCCGGGTG
P_AAF92065 1815 GTCACCCAGGCCCGCGAGGGCAACCTGCCCTCATTGCGCCCGCCCTGGCCCGGGTG
DNA44804 1667 CTCCCTGGCCGCGCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGGGGGGGGCCATG
P_AAF92065 1875 CTCCCTGGCCGCGCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGGGGGGGGCCATG
DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGGCTGGGCCCTGGAACGGAG
P_AAF92065 1935 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGGCTGGGCCCTGGAACGGAG
DNA44804 1787 GGAGTGAAGGTCCCTTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
P_AAF92065 1995 GGAGTGAAGGTCCCTTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804 1847 CCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCCTGGCCTCCAGTCA
P_AAF92065 2055 CCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804 1907 CCCCTCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT
P_AAF92065 2115 CCCCTCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT
DNA44804 1967 CTCAGCCAGTGAGATGCCAGGCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCA
P_AAF92065 2175 CTCAGCCAGTGAGATGCCAGGCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCA
DNA44804 2027 ACCTCGGGATGTGTCAGACAGGGCTGTGACCAAGCTGGGCCCTGTTCCCTCTGGA
P_AAF92065 2235 ACCTCGGGATGTGTCAGACAGGGCTGTGACCAAGCTGGGCCCTGTTCCCTCTGGA
DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
P_AAF92065 2295 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGGCAC
P_AAF92065 2355 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGAACGTGCAGTCCCTGGGCAC
DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA
P_AAF92065 2415 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA
DNA44804 2267 GGCGGACCCCTGGGGCCAGTGAAGGAAGGAAAGAGCAGAGGGAGAGCGGGTAGG
P_AAF92065 2475 GGCGGACCCCTGGGGCCAGTGAAGGAAGGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGACTCTAGTCTTGGCCCTGGGAAGCGAAGGAAACAAAAGAAACTGGAAAGGA

BLAST RESULTS A-29

P_AAF92065 2535 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAACTGGAAAGGA
DNA44804 2387 AGATGCTTAGGAACATGTTGCTTTAAAATATATATATTTATAAGAGATCCTT

P_AAF92065 2595 AGATGCTTAGGAACATGTTGCTTTAAA--ATATATATATTATAAGAGATCCTT
DNA44804 2447 TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA

P_AAF92065 2653 TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTA
DNA44804 2507 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA

P_AAF92065 2713 GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [P_AAF92065, seg 2/2]
Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

DNA44804 18 ACTCGAACGCAGTTGCTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGAC

P_AAF92065 1 ACTCGAACGCAGTTGCTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGAC
DNA44804 78 TGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCGCTCCGGGACAGAAGA

P_AAF92065 61 TGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCGCTCCGGGACAGAAGA
DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTACTGGCCCTGGGGCTGGGG

P_AAF92065 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTACTGGCCCTGGGGCTGGGG
DNA44804 198 TGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTTCTGCACTGCC

P_AAF92065 181 TGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTTCTGCACTGCC
DNA44804 258 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG

P_AAF92065 241 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG
DNA44804 318 AGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCTGCCGGGCTGCAGCTCC

P_AAF92065 301 AGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGGCTGCCGGGCTGCAGCTCC
DNA44804 378 TGGACCTGTCACAGAACAGATGCCAGCCTGC

P_AAF92065 361 TGGACCTGTCACAGAACAGATGCCAGCCTGC

>10 P_AAZ64959 Membrane-bound protein PRO1282 encoding cDNA. (2768 bp) [2 segs]
Score = 2127 (4216 bits), Expect = 0.0 [P_AAZ64959, seg 1/2]
Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand
+/-

DNA44804 407 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAAACAGCCTCCTGGCCCTGGAG

P_AAZ64959 615 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAAACAGCCTCCTGGCCCTGGAG
DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGGCGTGCAGCTGGCTGGCTGGGCTGCAG

P_AAZ64959 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGGCGTGCAGCTGGCTGGGCTGCAG

DNA44804	527	CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC *****
P_AAZ64959	735	CAGCTGGACGAGGGGCTTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCCGAC *****
DNA44804	587	AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCCCTGCGG *****
P_AAZ64959	795	AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCCTGACGCCCTGCGG *****
DNA44804	647	CTGGCCGGCAACACCCGATTGCCAGCTGCCGGCCCAGGACCTGCCGGCCTGGCTGCC *****
P_AAZ64959	855	CTGGCCGGCAACACCCGATTGCCAGCTGCCGGCCCAGGACCTGCCGGCCTGGCTGCC *****
DNA44804	707	CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCACCTCTCGGGC *****
P_AAZ64959	915	CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCTGGCACCTCTCGGGC *****
DNA44804	767	CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCAGCAACCCCTTAACACTGCGTGTGCC *****
P_AAZ64959	975	CTCTTCCCCCGCCTGCGCTGCTGGCAGCTGCCAGCAACCCCTTAACACTGCGTGTGCC *****
DNA44804	827	CTGAGCTGGTTGGCCCTGGTGCGAGAGCCACGTACACTGCCAGGCCCTGAGGAG *****
P_AAZ64959	1035	CTGAGCTGGTTGGCCCTGGTGCGAGAGCCACGTACACTGCCAGGCCCTGAGGAG *****
DNA44804	887	ACCGCCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTACTACGCC *****
P_AAZ64959	1095	ACCGCCTGCCACTTCCGCCAAGAACGCTGCCGGCTGCTCCTGGAGCTTACTACGCC *****
DNA44804	947	GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCCACCGAGGCCCGTGGTG *****
P_AAZ64959	1155	GACTTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCCACCGAGGCCCGTGGTG *****
DNA44804	1007	CGGGAGCCCACAGCCTTGTCTTAGCTTGCTCCTACCTGGCTTAGCCCCACAGGCCG *****
P_AAZ64959	1215	CGGGAGCCCACAGCCTTGTCTTAGCTTGCTCCTACCTGGCTTAGCCCCACAGGCCG *****
DNA44804	1067	GCCACTGAGGCCAGGCCGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG *****
P_AAZ64959	1275	GCCACTGAGGCCAGGCCGCCCTCCACTGCCAACCGACTGTAGGGCCTGTCCCCCAG *****
DNA44804	1127	CCCCAGGACTGCCAACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGGGACACGG *****
P_AAZ64959	1335	CCCCAGGACTGCCAACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGGGACACGG *****
DNA44804	1187	CACCACCTGGCGTGTGTTGTGCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG *****
P_AAZ64959	1395	CACCACCTGGCGTGTGTTGTGCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG *****
DNA44804	1247	GGGCAGGGGACACGGCCAGGCCACACCAGTCACGCCAGGCCACACGGTCCCTGACC *****
P_AAZ64959	1455	GGGCAGGGGACACGGCCAGGCCACACCAGTCACGCCAGGCCACACGGTCCCTGACC *****
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGCTGAGCGTACCTCCAG *****
P_AAZ64959	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGCTGAGCGTACCTCCAG *****

DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCGTCTCACCTATCGCAACCTATCGGCCCTGAT *****
P_AAZ64959	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCGTCTCACCTATCGCAACCTATCGGCCCTGAT *****
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGTGAGTACACGGTCACCCAGCTG *****
P_AAZ64959	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGTGAGTACACGGTCACCCAGCTG *****
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGGCCCGGGCGGGTGCCGGAG *****
P_AAZ64959	1695	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGGCCCGGGCGGGTGCCGGAG *****
DNA44804	1547	GGCGAGGAGGCCTGCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA *****
P_AAZ64959	1755	GGCGAGGAGGCCTGCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA *****
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATGGCCTGGCCCGGGTG *****
P_AAZ64959	1815	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATGGCCTGGCCCGGGTG *****
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGTGCGGTGGGGCAGCCTACTGTGTGCGGGGGCGGGCATG *****
P_AAZ64959	1875	CTCCTGGCCGCGCTGGCTGCGTGCGGTGGGGCAGCCTACTGTGTGCGGGGGCGGGCATG *****
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACGGAG *****
P_AAZ64959	1935	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAACGGAG *****
DNA44804	1787	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG *****
P_AAZ64959	1995	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG *****
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCCTCCAGTCA *****
P_AAZ64959	2055	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCCTCCAGTCA *****
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
P_AAZ64959	2115	CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT *****
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCC *****
P_AAZ64959	2175	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCC *****
DNA44804	2027	ACCTCGGGGATGTGTGAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA *****
P_AAZ64959	2235	ACCTCGGGGATGTGTGAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA *****
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
P_AAZ64959	2295	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
DNA44804	2147	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTCAGTCCCTGGGCAC *****
P_AAZ64959	2355	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTCAGTCCCTGGGCAC *****
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****

BLAST RESULTS A-32

P_AAZ64959 2415 *****GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGCTCTCCCACTCCA
DNA44804 2267 *****GGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
P_AAZ64959 2475 *****GGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 *****CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
P_AAZ64959 2535 *****CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
DNA44804 2387 *****AGATGCTTAGAACATGTTTGTCTTTAAAATATATATATATTTATAAGAGATCCTT
P_AAZ64959 2595 *****AGATGCTTAGAACATGTTTGTCTTTAAA--ATATATATATTTATAAGAGATCCTT
DNA44804 2447 *****TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAA
P_AAZ64959 2653 *****TCCCATTATTCTGGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAA
DNA44804 2507 *****GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA
P_AAZ64959 2713 *****GACAAACGATGATATGAAGGCCTTTGTAAGAAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [P_AAZ64959, seg 2/2]
Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGAC
P_AAZ64959 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGAC
DNA44804 78 TGAGGCCCGGGCTGCCCGCCCGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA
P_AAZ64959 61 TGAGGCCCGGGCTGCCCGCCCGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA
DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGG
P_AAZ64959 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGG
DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTCTGCACTGCC
P_AAZ64959 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTCTGCACTGCC
DNA44804 258 GCCAGGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG
P_AAZ64959 241 GCCAGGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG
DNA44804 318 AGAACGGCATCACCATGCTGACGCCAGCAGCTTGCCTGGGGCTGCCGGGCTGCAGCTCC
P_AAZ64959 301 AGAACGGCATCACCATGCTGACGCCAGCAGCTTGCCTGGGGCTGCCGGGCTGCAGCTCC
DNA44804 378 TGGACCTGTCACAGAACCAAGATGCCAGCCTGC
P_AAZ64959 361 TGGACCTGTCACAGAACCAAGATGCCAGCCTGC

>11 AX092284 Sequence 15 from Patent WO0116318. (2768 bp) [2 segs]
Score = 2127 (4216 bits), Expect = 0.0 [AX092284, seg 1/2]

BLAST RESULTS A -33

Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407, 615-2548, 2754, Strand +/+

DNA44804	407	CTGCGCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG *****
AX092284	615	CTGCGCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG *****
DNA44804	467	CCCGGCATCCTGGACACTGCCAACCTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG *****
AX092284	675	CCCGGCATCCTGGACACTGCCAACCTGGAGGCGCTGCGGCTGGCTGGTCTGGGCTGCAG *****
DNA44804	527	CAGCTGGACGAGGGGCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGAC *****
AX092284	735	CAGCTGGACGAGGGGCTTCAGCCGTTGCGAACCTCCACGACCTGGATGTGTCGAC *****
DNA44804	587	AACCAGCTGGAGCGAGTGCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCG *****
AX092284	795	AACCAGCTGGAGCGAGTGCACCTGTGATCCGAGGCCTCCGGGCTGACGCGCCTGCG *****
DNA44804	647	CTGGCCGCAACACCCGCATTGCCAGCTGCGGCCAGGACCTGGCGGCCCTGGCTGCC *****
AX092284	855	CTGGCCGCAACACCCGCATTGCCAGCTGCGGCCAGGACCTGGCGGCCCTGGCTGCC *****
DNA44804	707	CTGCAGGAGCTGGATGTGAGCAAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTGGC *****
AX092284	915	CTGCAGGAGCTGGATGTGAGCAAACCTAACGCTGCAGGCCCTGCCTGGCGACCTCTGGC *****
DNA44804	767	CTCTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTAAC TGCGTGTGCCCC *****
AX092284	975	CTCTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTAAC TGCGTGTGCCCC *****
DNA44804	827	CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGGCAGGCCCTGAGGAG *****
AX092284	1035	CTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGGCAGGCCCTGAGGAG *****
DNA44804	887	ACCGCGCTGCCACTTCCCGCCAAGAACGCTGGCGGCCCTGGAGCTTGACTACGCC *****
AX092284	1095	ACCGCGCTGCCACTTCCCGCCAAGAACGCTGGCGGCCCTGGAGCTTGACTACGCC *****
DNA44804	947	GACTTGGCTGCCAGCCACCACACCACAGGCCACAGTGCCACCAAGGAGGCCCTGGTG *****
AX092284	1155	GACTTGGCTGCCAGCCACCACACCACAGGCCACAGTGCCACCAAGGAGGCCCTGGTG *****
DNA44804	1007	CGGGAGCCCACAGCCTTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGGCCG *****
AX092284	1215	CGGGAGCCCACAGCCTTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGGCCG *****
DNA44804	1067	GCCACTGAGGCCAGCCGCCCTCCACTGCCACCGACTGTAGGGCTGTCCCCCAG *****
AX092284	1275	GCCACTGAGGCCAGCCGCCCTCCACTGCCACCGACTGTAGGGCTGTCCCCCAG *****
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGGGACACGG *****
AX092284	1335	CCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGGGACACGG *****
DNA44804	1187	CACCACCTGGCGTGCTGTGCCCCGAAGGCTCACGGCCTGTACTGTGAGAGCCAGATG *****

BLAST RESULTS A-34

AX092284	1395	CACCACCTGGCGTGCTTGTGCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
AX092284	1455	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
AX092284	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTACACCTATCGAACCTATGGGCCCTGAT
AX092284	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTACACCTATCGAACCTATGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCAGCTG
AX092284	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCAGCTG
DNA44804	1487	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCTTGGGCCCGGGCGGGTGCCGGAG
AX092284	1695	CGGCCAACGCCACTTACTCCGTCTGTGTATGCCTTGGGCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
AX092284	1755	GGCGAGGAGGCCTGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGTCCATTGCGCCGCCCTGGCCCGGTG
AX092284	1815	GTCACCCAGGCCCGCGAGGGCAACCTGCCGTCCATTGCGCCGCCCTGGCCCGGTG
DNA44804	1667	CTCCTGGCCCGCCTGGCTGCCGTGGGGCAGCCTACTGTGTGCGGCGGGGGCGGCCATG
AX092284	1875	CTCCTGGCCCGCCTGGCTGCCGTGGGGCAGCCTACTGTGTGCGGCGGGGGCGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAG
AX092284	1935	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGCCAGGGCTGGCCCTGGAACTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
AX092284	1995	GGAGTGAAGGTCCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCTCCAGTCA
AX092284	2055	CCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCTCCAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT
AX092284	2115	CCCCTCCACGCAAAGCCCTACATCTAACGCCAGAGAGACAGGGCAGCTGGGCCGGCT
DNA44804	1967	CTCAGCCAGTGAAGATGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
AX092284	2175	CTCAGCCAGTGAAGATGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCAACAGCTGGGCCCTGTTCCCTCTGGA
AX092284	2235	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCAACAGCTGGGCCCTGTTCCCTCTGGA

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DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA *****
AX092284	2295	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA *****
DNA44804	2147	ACCGAGTGCCTATGAGGAACAGTGTCGCCCTGCCCTCCGAAACGTGCAGTCCCTGGGCAC *****
AX092284	2355	ACCGAGTGCCTATGAGGAACAGTGTCGCCCTGCCCTCCGAAACGTGCAGTCCCTGGGCAC *****
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****
AX092284	2415	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA *****
DNA44804	2267	GGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGG *****
AX092284	2475	GGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGG *****
DNA44804	2327	CGGCTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA *****
AX092284	2535	CGGCTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGA *****
DNA44804	2387	AGATGCTTTAGGAACATGTTTGCTTTAAAATATATATATTATAAGAGATCCTT *****
AX092284	2595	AGATGCTTTAGGAACATGTTTGCTTTAAA--ATATATATATTATAAGAGATCCTT *****
DNA44804	2447	TCCCATTATTCTGGGAAGATGTTTCAAACACTCAGAGACAAGGACTTGGTTTGAA *****
AX092284	2653	TCCCATTATTCTGGGAAGATGTTTCAAACACTCAGAGACAAGGACTTGGTTTGAA *****
DNA44804	2507	GACAAACGATGATATGAAGGCCTTTGTAAGAAAAATAAAA *****
AX092284	2713	GACAAACGATGATATGAAGGCCTTTGTAAGAAAAATAAAA *****

Score = 389 (771 bits), Expect = 0.0 [AX092284, seg 2/2]

Identities = 392/393 (99%), at 18,1-410,393, Strand +/-

DNA44804	18	ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC *****
AX092284	1	ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC *****
DNA44804	78	TGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA *****
AX092284	61	TGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTCCGGGACAGAAGA *****
DNA44804	138	TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCCTGCTACTGGCCCTGGGCCTGGGG *****
AX092284	121	TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCCTGCTACTGGCCCTGGGCCTGGGG *****
DNA44804	198	TGCAGGGCTGCCCATCCGGCTGCCAGTGCAAGCCAGCCACAGACAGTCTTCTGCACTGCC *****
AX092284	181	TGCAGGGCTGCCCATCCGGCTGCCAGTGCAAGCCAGCCACAGACAGTCTTCTGCACTGCC *****
DNA44804	258	GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG *****
AX092284	241	GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTG *****
DNA44804	318	AGAACGGCATCACCATGCTCGACGCAAGCAGCTTGCCGGCTGCCGGCCTGCAGCTCC *****

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AX092284 301 AGAACGGCATCACCATGCTCGACGCAGGCAGCTTGCCGGCCTGCCGGCCTGCAGCTCC
DNA44804 378 TGGACCTGTACAGAACCGAGATGCCAGCCTGC

AX092284 361 TGGACCTGTACAGAACCGAGATGCCAGCCTGC

>12 P_AAC69514 Human secreted protein gene 3 clone HSYAV50. DNA, PAT 31-JAN-2001 (2801 bp) [2 segs]
Score = 2065 (4094 bits), Expect = 0.0 [P_AAC69514, seg 1/2]
Identities = 2135/2149 (99%), Gaps = 7/2149 (0%), at 407,650-2555,2791, Strand +/+

DNA44804 407 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

P_AAC69514 650 CTGCGCCTGCCCGCCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCCGCTGGCTGGCTGGCTGGGCTGCAG

P_AAC69514 710 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCCGCTGGCTGGCTGGGCTGCAG

DNA44804 527 CAGCTGGACGAGGGGCTTCAGCCGTTGCCAACCTCCACGACCTGGATGTGTCCGAC

P_AAC69514 770 CAGCTGGACGAGGGGCTTCAGCCGTTGCCAACCTCCACGACCTGGATGTGTCCGAC

DNA44804 587 AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCC

P_AAC69514 830 AACCAAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGCGCTGACGCGCCTGCC

DNA44804 647 CTGGCCGGCAACACCCGATTGCCAGCTGCCGCCCCAGGACCTGGCCGGCCTGGCTGCC

P_AAC69514 890 CTGGCCGGCAACACCCGATTGCCAGCTGCCGCCCCAGGACCTGGCCGGCCTGGCTGCC

DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCGACCTCTCGGGC

P_AAC69514 950 CTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGCCCTGCCGACCTCTCGGGC

DNA44804 767 CTCTCCCCCGCCTGCCAGCTGGCAGCTGCCCAACCCCTTAACACTGCC

P_AAC69514 1010 CTCTCCCCCGCCTGCCAGCTGGCAGCTGCCCAACCCCTTAACACTGCC

DNA44804 827 CTGAGCTGGTTGGCCCTGGGTGCGCAGAGGCCACGTACACTGCCAGCCCTGAGGAG

P_AAC69514 1070 CTGAGCTGGTTGGCCCTGGGTGCGCAGAGGCCACGTACACTGCCAGCCCTGAGGAG

DNA44804 887 ACACGCTGCCACTTCCCAGCCAAAGAACGCTGCCAGCTGCCAGCTAACACTGCC

P_AAC69514 1130 ACACGCTGCCACTTCCCAGCCAAAGAACGCTGCCAGCTGCCAGCTAACACTGCC

DNA44804 947 GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACACCACGAGGCCCTGGT

P_AAC69514 1190 GACTTGGCTGCCAGCCACCACACCACAGCCACAGTGCCACACCACGAGGCCCTGGT

DNA44804 1007 CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGGCC

P_AAC69514 1250 CGGGAGCCCACAGCCTGTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGGCC

DNA44804 1067 GCCACTGAGGCCCGAGCCCCAGCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

P_AAC69514 1310 GCCACTGAGGCCCGAGCCCCAGCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

DNA44804 1127 CCCCAGGACTGCCAACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG

P_AAC69514 1370 CCCCAGGACTGCCAACCGTCCACCTGCCTCAATGGGGCACATGCCACCTGGGACACGG

DNA44804 1187 CACCACCTGGCGTGCTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

P_AAC69514 1430 CACCACCTGGCGTGCTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGGTCCCTGACC

P_AAC69514 1490 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACCGGTCCCTGACC

DNA44804 1307 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCCTGGGGCTGCAGCGCTACCTCCAG

P_AAC69514 1550 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCCTGGGGCTGCAGCGCTACCTCCAG

DNA44804 1367 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGAT

P_AAC69514 1610 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGAACCTATCGGGCCCTGAT

DNA44804 1427 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG

P_AAC69514 1670 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGAGTACACGGTCACCCAGCTG

DNA44804 1487 CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCGGCGGGTGCCGGAG

P_AAC69514 1730 CGGCCAACGCCACTTACTCCGTCTGTGTATGCCCTGGGCCGGCGGGTGCCGGAG

DNA44804 1547 GGCGAGGAGGCCTGCCGGGAGGCCATACACCCCGCCAGCGTCCACTCCAACCACGCCCA

P_AAC69514 1790 GGCGAGGAGGCCTGCCGGGAGGCCATACACCCCGCCAGCGTCCACTCCAACCACGCCCA

DNA44804 1607 GTCACCCAGGCCCGCGAGGGCAACCTGCCCTCATTGCCCGCCCTGGCCCGGTG

P_AAC69514 1850 GTCACCCAGGCCCGCGAGGGCAACCTGCCCTCATTGCCCGCCCTGGCCCGGTG

DNA44804 1667 CTCCTGGCCCGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGCGGCCATG

P_AAC69514 1910 CTCCTGGCCCGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGCGGCCATG

DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACCTGGAG

P_AAC69514 1970 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACCTGGAG

DNA44804 1787 GGAGTGAAGGTCCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AAC69514 2030 GGAGTGAAGGTCCCCTGGAGGCCAGGCCGAAGGCAACAGA-GGCGGTGGAGAGGCCCTG

DNA44804 1847 CCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCTCCAGTCA

P_AAC69514 2089 CCCAGCGGGCTGAGTGTGAGTGCCACTCATGGCTT-CCAAGGCCTGGCCT-CAGTCA

DNA44804 1907 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCCGGCT

BLAST RESULTS A-38

***** * *****
P_AAC69514 2147 CCCCTCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCT-GGGCCGGG-T
DNA44804 1967 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

P_AAC69514 2205 TTCAGCCAGTGAGAT-GCCAGCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804 2027 ACCTCGGGGATGTGTCAGACAGGGCTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

P_AAC69514 2264 ACCTCGGGGATGTGTCAGACAGGGCTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGCCCCAGCTGACGAGCCCTAACGTCCCCAGA

P_AAC69514 2324 CCTCGGTCTCCTCATCTGTGAGATGCTGTGCCCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCGCCCTGCCCTCCGAAACGTGCAAGTCCCTGGGCAC

P_AAC69514 2384 ACCGAGTGCCTATGAGGACAGTGTCGCCCTGCCCTCCGAAACGTGCAAGTCCCTGGGCAC
DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA

P_AAC69514 2444 GGCGGG-CCTGCCATGTGCTGGTAACGCATGCCCTGGGCCCTGCTGGCTCTCCACTCCA
DNA44804 2267 GGCGGACCCCTGGGGGCCAGTGAAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG

P_AAC69514 2503 GGCGGACCCCTGGGGGCCAGTGAAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGACTCTAGTCTTGGCCCCAGGAAGCGAACAAAAGAAAAGTGGAAAGGA

P_AAC69514 2563 CGGCTGTGACTCTAGTCTTGGCCCCAGGAAGCGAACAAAAGAAAAGTGGAAAGGA
DNA44804 2387 AGATGCTTAGAACATGTTGCTTTAAATATAATATATTATAAGAGATCCTT

P_AAC69514 2623 AGATGCTTAGAACATGTTGCTTTAAATATAATATTATAAGAGATCCTT
DNA44804 2447 TCCCATTATTCTGGAAAGATGTTTCAAACCTCAGAGACAAGGACTTGGTTTGAA

P_AAC69514 2683 TCCCATTATTCTGGAAAGATGTTTCAAACCTCAGAGACAAGGACTTGGTTTGAA
DNA44804 2507 GACAAACGATGATATGAAGGCCTTGTAAAGAAAAAAATAAAAAAAAAAAA

P_AAC69514 2743 GACAAACGATGATATGAAGGCCTTGTAAAGAAAAAAATAAAAAAAAAAAA

Score = 406 (805 bits), Expect = 0.0 [P_AAC69514, seg 2/2]
Identities = 409/410 (99%), at 1,19-410,428, Strand +/-

DNA44804 1 GGGGCGGGTGGACGCAGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTGGGCC

P_AAC69514 19 GGGGCGGGTGGACGCAGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTGGGCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCCGCCGGCTCCCTGCGCCGCCGCG

P_AAC69514 79 GACCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCCGCCGGCTCCCTGCGCCGCCGCG
DNA44804 121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCCTGCTACT

P_AAC69514 139 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCCTGCTACT

BLAST RESULTS A-39

DNA44804	181	GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC *****
P_AAC69514	199	GGCCCTGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC *****
DNA44804	241	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCGACACGGT *****
P_AAC69514	259	AGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCGACACGGT *****
DNA44804	301	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCAGCTTGCCGGCCT *****
P_AAC69514	319	GGGGCTGTACGTCTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCAGCTTGCCGGCCT *****
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGC *****
P_AAC69514	379	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACAGATGCCAGCCTGC

(B)

Wed Aug 29 08:13:54 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
 /home/ruby/va/Molbio/carpenda/tempids/p1.DNA44804 (598 aa)



Sequences producing High-scoring Segment Pairs:			
		Score	Match Pct E-val
1	P_AAB01322 Human PRO357 polypeptide - Homo sapiens.	3135	598 100 0.0
2	P_AAY93691 novel polypeptide PRO357 - Homo sapiens.	3135	598 100 0.0
3	P_AAY06484 Human tumour-associated protein PRO357 -	3135	598 100 0.0
4	P_AAY17831 Human PRO357 protein sequence - Homo sapi	3126	597 100 0.0
5	P_AAB65166 Human PRO1282 (UNQ652) protein sequence S	2946	582 86 0.0
6	P_AAB87533 Human PRO1282 - Homo sapiens.	2946	582 86 0.0
7	P_AAB07428 leucine-rich surface glycoprotein (LRSG)	2946	582 86 0.0
8	CAC49977.1 unnamed protein product - Homo sapiens	2941	581 86 0.0
9	P_AAB38400 Fragment of human secreted protein encode	2792	560 83 0.0
10	P_AAB38323 Human secreted protein encoded by gene 3	2792	560 83 0.0
11	P_AAY66643 Membrane-bound protein PRO1282 - Homo sap	2405	502 75 0.0

>1 P_AAB01322 Human PRO357 polypeptide - Homo sapiens. (598 aa) [1 seg]
 Score = 3135 (1212 bits), Expect = 0.0
 Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804 1 MCSRVPLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

 P_AAB01322 1 MCSRVPLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

 DNA44804 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLHSNSSLALEPGILDNTANVE

 P_AAB01322 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLHSNSSLALEPGILDNTANVE

 DNA44804 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPPIRGLRGLTRLRLAGNTRIAQL

 P_AAB01322 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPPIRGLRGLTRLRLAGNTRIAQL

 DNA44804 181 RPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPNFNCVCPLSWFGPWRE

 P_AAB01322 181 RPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPNFNCVCPLSWFGPWRE

 DNA44804 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

 P_AAB01322 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

 DNA44804 301 APTWLSPTAPATEAPSPPSTAPPTVGVPVPQPDCCPPSTCLNGGTCHLGTRHHLACLCPEG

 P_AAB01322 301 APTWLSPTAPATEAPSPPSTAPPTVGVPVPQPDCCPPSTCLNGGTCHLGTRHHLACLCPEG

 DNA44804 361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTIGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR

 P_AAB01322 361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTIGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR

 DNA44804 421 LTYRNLSGPDKRLVTLLPASLAEYTVTQLRPNATYSVCVMPGPGRVPEGEAACGEAHT

 P_AAB01322 421 LTYRNLSGPDKRLVTLLPASLAEYTVTQLRPNATYSVCVMPGPGRVPEGEAACGEAHT

 DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGQV

 P_AAB01322 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGQV

BEST RESULTS B-1

BEST RESULTS B-2

DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

P_AAB01322 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>2 P_AAY93691 novel polypeptide PRO357 - Homo sapiens. (598 aa) [1 seg]
Score = 3135 (1212 bits), Expect = 0.0
Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804 1 MCSRVPLLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

P_AAY93691 1 MCSRVPLLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

DNA44804 61 ENGITMLDASSFAGLPGQLLDSLQNQIASLRLPRLLLDLSHNSLLALEPGILDNTANVE

P_AAY93691 61 ENGITMLDASSFAGLPGQLLDSLQNQIASLRLPRLLLDLSHNSLLALEPGILDNTANVE

DNA44804 121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

P_AAY93691 121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPWRE

P_AAY93691 181 RPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPWRE

DNA44804 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

P_AAY93691 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

DNA44804 301 APTWLSPTAPATEAPSPPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG

P_AAY93691 301 APTWLSPTAPATEAPSPPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG

DNA44804 361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR

P_AAY93691 361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR

DNA44804 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT

P_AAY93691 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT

DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQV

P_AAY93691 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQV

DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

P_AAY93691 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>3 P_AAY06484 Human tumour-associated protein PRO357 - Homo sapiens. (598 aa) [1 seg]
Score = 3135 (1212 bits), Expect = 0.0
Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804 1 MCSRVPLLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

P_AAY06484 1 MCSRVPLLLPLLLLALGPGVQGCPSPGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

DNA44804 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILD TANVE

P_AAY06484 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILD TANVE

DNA44804 121 ALRLAGLGLQQLD EGLFSRLRNLDL DVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

P_AAY06484 121 ALRLAGLGLQQLD EGLFSRLRNLDL DVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLA AARNPFCVCPLSWFGPWVRE

P_AAY06484 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLA AARNPFCVCPLSWFGPWVRE

DNA44804 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

P_AAY06484 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

DNA44804 301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHACLCPEG

P_AAY06484 301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHACLCPEG

DNA44804 361 FTGLYCESQM GQGTRPSPTPVT PRPPRSLT LGIEPVSP TS LRVGL QRYL QGSSVQLRSLR

P_AAY06484 361 FTGLYCESQM GQGTRPSPTPVT PRPPRSLT LGIEPVSP TS LRVGL QRYL QGSSVQLRSLR

DNA44804 421 LT YRNLSGPDKRLVT LRLPASLA EYTVT QLRPNAT YS CVMPLGPGRVPEGEEACGEAHT

P_AAY06484 421 LT YRNLSGPDKRLVT LRLPASLA EYTVT QLRPNAT YS CVMPLGPGRVPEGEEACGEAHT

DNA44804 481 PPAVHSN HAPVTQAREGNLPLL IAPALAA VLLA ALAA VGAAYCVR GRAMAAA QDKGQV

P_AAY06484 481 PPAVHSN HAPVTQAREGNLPLL IAPALAA VLLA ALAA VGAAYCVR GRAMAAA QDKGQV

DNA44804 541 GPGAGPLELEGVKVPL EPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

P_AAY06484 541 GPGAGPLELEGVKVPL EPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>4 P_AAY17831 Human PRO357 protein sequence - Homo sapiens. (598 aa) [1 seg]
Score = 3126 (1208 bits), Expect = 0.0
Identities = 597/598 (99%), Positives = 597/598 (99%), at 1,1-598,598

DNA44804 1 MCSRVPLLP LLLLALGP GVQG CP SG CQ CSQP QT VFCT ARQ GTT VPR DVPP DT VG LYVF

P_AAY17831 1 MCSRVPLLP LLLLALGP GVQG CP SG CQ CSQP QT VFCT ARQ GTT VPR DVPP DT VG LYVE

DNA44804 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILD TANVE

P_AAY17831 61 ENGITMDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILD TANVE

DNA44804 121 ALRLAGLGLQQLD EGLFSRLRNLDL DVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

P_AAY17831 121 ALRLAGLGLQQLD EGLFSRLRNLDL DVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLA AARNPFCVCPLSWFGPWVRE

P_AAY17831 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLA AARNPFCVCPLSWFGPWVRE

DNA44804 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL

BLAST RESULTS BrA

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*****
P_AAY17831 241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL
DNA44804 301 APTWLSPTAPATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG
*****
P_AAY17831 301 APTWLSPTAPATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG
DNA44804 361 FTGLYCESQMGQQGTRPSPTPVTPRPPRSLTGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR
*****
P_AAY17831 361 FTGLYCESQMGQQGTRPSPTPVTPRPPRSLTGIEPVSPSTSRLVGLQRYLQGSSVQLRSLR
DNA44804 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT
*****
P_AAY17831 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT
DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAAYCVRGRAMAAAQDKGQV
*****
P_AAY17831 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAAYCVRGRAMAAAQDKGQV
DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
*****
P_AAY17831 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>5 P_AAB65166 Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52 - Homo (673
aa) [1 seg]
Score = 2946 (1139 bits), Expect = 0.0
Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at
1,1-598,673

DNA44804 1 MCSRVPLLPLLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
*****
P_AAB65166 1 MCSRVPLLPLLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
DNA44804 61 EN-----GITMLDAS-----SF
** * . ** *
P_AAB65166 61 ENGITMLDAGSFAGLPGLQLLDSLQNQIASLPSGVFQPLANLSNLDTANRLHEITNETF
DNA44804 73 AGLPGLQLLDSLQNQIAS-----LRLPRLLLDLHSNS
** * . * * . *
P_AAB65166 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLDLHSNS
DNA44804 106 LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIIRGLRG
*****
P_AAB65166 181 LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIIRGLRG
DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPF
*****
P_AAB65166 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPF
DNA44804 226 NCVCPLSWFGP WVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPT
*****
P_AAB65166 301 NCVCPLSWFGP WVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPT
DNA44804 286 TRPVVREPTALSSLAPTWLSPTAPATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTC
*****
P_AAB65166 361 TRPVVREPTALSSLAPTWLSPTAPATEAPSPPSTAPPTVGVPQPQDCPPSTCLNGGTC

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BLAST RESULTS B-5

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DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQQGTRPSPTPVRPPRSLTGIEPVSPSLRVGL
*****  

P_AAB65166 421 HLGTRHHLACLCPEGFTGLYCESQMGQQGTRPSPTPVRPPRSLTGIEPVSPSLRVGL  

DNA44804 406 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAETVTQLRPNATYSVCVMPLGP
*****  

P_AAB65166 481 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAETVTQLRPNATYSVCVMPLGP  

DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAVCVR
*****  

P_AAB65166 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAVCVR  

DNA44804 526 RGRAMAAAQDKGQVQPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG
*****  

P_AAB65166 601 RGRAMAAAQDKGQVQPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  

DNA44804 586 PGLQSPLHAKPYI
*****  

P_AAB65166 661 PGLQSPLHAKPYI

>6 P_AAB87533 Human PRO1282 - Homo sapiens. (673 aa) [1 seg]
Score = 2946 (1139 bits), Expect = 0.0
Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at
1,1-598,673

DNA44804 1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
*****  

P_AAB87533 1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  

DNA44804 61 EN-----GITMLDAS-----SF
**      * . ** *
P_AAB87533 61 ENGITMLDAGSFAGLPGLQLLDSQNQIASLPSGVFQPLANLSNLDTANRLHEITNETF  

DNA44804 73 AGLPGLQLLDSQNQIAS-----LRLPRLLLLDLHNS
**      * . ** .
P_AAB87533 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLELKQDNELRALPPLRLPRLLLLLDLHNS  

DNA44804 106 LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRG
*****  

P_AAB87533 181 LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRG  

DNA44804 166 LTRLRLLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLLLAAARNPF
*****  

P_AAB87533 241 LTRLRLLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLLLAAARNPF  

DNA44804 226 NCVCPLSWFGP WVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATT TATVPT
*****  

P_AAB87533 301 NCVCPLSWFGP WVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATT TATVPT  

DNA44804 286 TRPVVREPTALSSLAPTWLSPTAPATEAPS PPP STAPPTVGPVPQPQDCPPSTCLNGGTC
*****  

P_AAB87533 361 TRPVVREPTALSSLAPTWLSPTAPATEAPS PPP STAPPTVGPVPQPQDCPPSTCLNGGTC  

DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQQGTRPSPTPVRPPRSLTGIEPVSPSLRVGL
*****  

P_AAB87533 421 HLGTRHHLACLCPEGFTGLYCESQMGQQGTRPSPTPVRPPRSLTGIEPVSPSLRVGL

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BLAST RESULTS B-U

DNA44804 406 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

P_AAB87533 481 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAVCVR

P_AAB87533 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAVCVR

DNA44804 526 RGRAMAQAQDKGVQVPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

P_AAB87533 601 RGRAMAQAQDKGVQVPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

DNA44804 586 PGLQSPLHAKPYI

P_AAB87533 661 PGLQSPLHAKPYI

>7 P_AAB07428 leucine-rich surface glycoprotein (LRSG) - Homo sapiens. (673 aa)
[1 seg]
Score = 2946 (1139 bits), Expect = 0.0
Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at
1,1-598,673

DNA44804 1 MCSRVPLLPLLLLALGPGVQGCPSCQCSQPQTVFCTARQTTVPRDVPPDTVGLYVF

P_AAB07428 1 MCSRVPLLPLLLLALGPGVQGCPSCQCSQPQTVFCTARQTTVPRDVPPDTVGLYVF

DNA44804 61 EN-----GITMLDAS-----SF
** * . * * * . * . *
P_AAB07428 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF

DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLDLSHNS
** * . * * . * . *
P_AAB07428 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLDLSHNS

DNA44804 106 LLALEPGILDGTANVEALRLAGLQLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRG

P_AAB07428 181 LLALEPGILDGTANVEALRLAGLQLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRG

DNA44804 166 LTRLRLLAGNTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPF

P_AAB07428 241 LTRLRLLAGNTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPF

DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPT

P_AAB07428 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPT

DNA44804 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC

P_AAB07428 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC

DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTVTPRPPRSLTIGIEPVSPSLRVGL

P_AAB07428 421 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTVTPRPPRSLTIGIEPVSPSLRVGL

DNA44804 406 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

P_AAB07428 481 QRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

BEST RESULTS B-7

BLAST RESULTS B-8

BLAST RESULTS B-9

BLAST RESULTS D-10

P_AAB38323 661 -WPQSPLHAKPYI

>11 P_AAY66643 Membrane-bound protein PRO1282 - Homo sapiens. (611 aa) [1 seg]
Score = 2405 (931 bits), Expect = 0.0
Identities = 502/673 (74%), Positives = 512/673 (75%), Gaps = 137/673 (20%), at 1,1-598, 611

DNA44804	1	MCSRVPLLLPLLLLLALGPGVQGCPGCGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF	*****
P_AAY66643	1	MCSRVPLLLPLLLLLALGPGVQGCPGCGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF	*****
DNA44804	61	EN-----GITMLDAS-----SF	** . * * * . *
P_AAY66643	61	ENGITMLDAGSFAGLPGQLLLDSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF	*****
DNA44804	73	AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS	** . * * * . * *****
P_AAY66643	121	RGLRRRLERLYLGKNRIRHIQPGAFDTLDRLELKQDNELRALPPLRPRLLLLDLSHNS	*****
DNA44804	106	LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDL DVSDNQLERVPPVIRGLRG	*****
P_AAY66643	181	LLALEPGILD TANVEALRLAGLGLQQLDEGLFSRLRNLDL DVSDNQLERVPPVIRGLRG	*****
DNA44804	166	LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPF	*****
P_AAY66643	241	LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPF	*****
DNA44804	226	NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLEDYADFGCPATTTATVPT	*****
P_AAY66643	301	NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLEDYADFGCPATTTATVPT	*****
DNA44804	286	TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPP TVGPVPQPQDCPPSTCLNGGTC	*****
P_AAY66643	361	TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPP TVGPVPQPQDCPPSTCLNGGTC	*****
DNA44804	346	H LGTRHHLA CLCP EGFT GLYCESQM GQGTRPSPTVTPRPPRSLT LGIEPVSPS TSLRVGL	*****
P_AAY66643	421	H LGTRHHLA CLCP EGFT GLYCESQM GQGTRPSPTVTPRPPRSLT LGIEPVSPS TSLRVGL	*****
DNA44804	406	Q RYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLA EYTVTQLRPNATYSVCVMPLGP	***** . * *** *
P_AAY66643	481	Q RYLQGSSVQLRSLRLVHSN-----HAPVTQAR-----	*****
DNA44804	466	GRVPEGE EACGEAHTPPAVHSNHAPVTQAREGNLPLLIA P A L A A V I L A A L A A V G A A Y C V R	* . * . ** * * *** . *****
P_AAY66643	509	-----EGNLPLLI----APA-----L A A V L L A A L -----AAVGAAYCVR	*****
DNA44804	526	R GRAMAAA QDKGQVGP GAGPLELEG V KV PLEPGPKATEGGGEALPSGSECEVPLMGFPG	*****
P_AAY66643	539	R GRAMAAA QDKGQVGP GAGPLELEG V KV PLEPGPKATEGGGEALPSGSECEVPLMGFPG	*****
DNA44804	586	P GLQSPLHAKPYI	*****
P_AAY66643	599	P GLQSPLHAKPYI	*****